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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/287,632DATE: 06/30/1999
TIME: 14:41:48

Input Set: I287632.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: WATERHOUSE, Peter Michael
2 WANG, Ming-Bo
3 GRAHAM, Michael Wayne
4 <120> TITLE OF INVENTION: METHODS AND MEANS FOR OBTAINING MODIFIED PHENOTYPES
5 <130> FILE REFERENCE: 021565-060
6 <140> CURRENT APPLICATION NUMBER: US/09/287,632
7 <141> CURRENT FILING DATE: 1999-04-07
8 <150> EARLIER APPLICATION NUMBER: US 09/127,735
9 <151> EARLIER FILING DATE: 1998-08-03
10 <150> EARLIER APPLICATION NUMBER: US 09/056,767
11 <151> EARLIER FILING DATE: 1998-04-08
12 <160> NUMBER OF SEQ ID NOS: 7
13 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO 1
15 <211> LENGTH: 854
16 <212> TYPE: DNA
17 <213> ORGANISM: Potato virus Y
18 <220> FEATURE:
19 <223> OTHER INFORMATION: fragment of the NIa ORF
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22 gcattgccaa atttcctgag agagagttcg agctaaggca gactgggcca gctgtagaag 120
23 tcgacgtgaa ggacatacca gcacaggagg tggaaacatga agctaaatcg ctcatgagag 180
24 gcttgagaga cttcaaccca attgcccata cagttttagt gctgaaagta tctgttgaat 240
25 atgggacatc agagatgtac ggttttggat ttggagcgta cataatagcg aaccaccatt 300
26 tgttcaggag ttataatggt tccatggagg tacgatccat gcacggtaca ttcagggtaa 360
27 agaatctaca cagttttagc gttctgccaa ttaaaggtag ggacatcatc ctcatataaa 420
28 tgccaaaaga tttccctgtc tttccacaga aattgcattt ccgagctcct acacagaacg 480
29 aaagaatttg tttagttgga accaactttc aggagaagta tgcacgctcg atcatcacag 540
30 aagcaagcac tacttacaat ataccaggca gcacattctg gaagcattgg attgaaacag 600
31 ataattggaca ctgtggacta ccagtggtga gcactgccga tggatgtcta gtcggaattc 660
32 acagtttggc aaacaatgca cacaccacga actactactc agccttcgat gaagattttg 720
33 aaagcaagta cctccgaacc aatgagcaca atgaatgggt caagtcttgg atttataatc 780
34 cagacacagt gttgtggggc ccgttgaaac ttaaagacag cactcctaaa gggttattta 840
35 aaacaacaaa gctt 854
36 <210> SEQ ID NO 2
37 <211> LENGTH: 2186
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Description of Artificial Sequence: coding region
42 of the Gusd CoP construct
43 <220> FEATURE:
44 <221> NAME/KEY: misc_structure

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45 <222> LOCATION: (..)
46 <223> OTHER INFORMATION: deficient Gus coding region
47 <220> FEATURE:
48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: (..) (2186)
50 <223> OTHER INFORMATION: antisense to the 5' end of the Gus coding region
51 <400> SEQUENCE: 2
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53      ttcagtctgg atcgcgaaaa ctgtggaatt gatcagcgtt ggtgggaaag cgcgttacaa 120
54      gaaagccggg caattgctgt gccaggcagt tttaacgata agttcgccga tgcagatatt 180
55      cgtaattatg cgggcaacgt ctggtatcag cgcgaagtct ttataccgaa aggttgggca 240
56      ggccagcgta tcgtgctgcy tttcgatgcy gtcaactcatt acggcaaagt gtgggtcaat 300
57      aatcaggaag tgatggagca tcagggcggc tatacgccat ttgaagccga tgtcacgccc 360
58      tatgttattg ccgggaaaaa tgtacgtatc accgtttgtg tgaacaacga actgaactgg 420
59      cagactatcc cgcgggaat ggtgattacc gacgaaaacg gcaagaaaaa gcagtcttac 480
60      ttccatgatt tctttaacta tgccggaatc catcgacgcy taatgctcta caccacgccc 540
61      aacacctggg tggacgatat ctacccgctt cgcgtcggca tccggtcagt ggcagtgaag 600
62      ggcgaaacgt tcctgattaa ccacaaacgg ttctacttta ctggctttgg tcgtcatgaa 660
63      gatgcggact tgcgtggcaa aggattcgat aacgtgctga tgggtgcacga ccacgcatta 720
64      atggactgga ttggggccaa ctctaccgt accctgcatt acccttacgc tgaagagatg 780
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67      gaggcagtca acggggaaac tcagcaagcg cacttacagg cgattaaaga gctgatagcg 960
68      cgtgacaaaa accaccaag cgtggtgatg tggagtattg ccaacgaacc ggatacccg 1020
69      ccgcaagggtg cacgggaata tttcgcgcca ctggcggaag caacgcgtaa actcgacccg 1080
70      acggtccga tcacctgctg caatgtaatg ttctgcgacg ctcacaccga taccatcagc 1140
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75      gatcgctca gcgccgtcgt cggtaaacag gtatggaatt tcgccgattt tgcgacctcg 1440
76      caaggcatat tgcgcgttgg cggtaacaag aaagggatct tcaactcgca ccgcaaaccg 1500
77      aagtcggcgg cttttctgct gcaaaaacgc tggactggca tgaacttcgg tgaaaaaccg 1560
78      cagcaggagg gcaaacaatg aaacagacgc gtggttacag tcttgcgcga catgcgtcac 1620
79      cacggtgata tcgtccaccc aggtgttcgg cgtggtgtag agcatacgtc gcgatggatt 1680
80      ccggcatagt taaagaaatc atggaagtaa gactgctttt tcttgccgtt ttcgtcggta 1740
81      atcaccattc ccggcgggat agtctgccag ttcagttcgt tgttcacaca aacggtgata 1800
82      cgtacacttt tcccggcaat aacatacggc gtgacatcgg cttcaaatgg cgtatagccg 1860
83      ccctgatgct ccatcacttc ctgattattg acccacactt tgcgtaatg agtgaccgca 1920
84      tcgaaacgca gcacgatacg ctggcctgcc caacctttcg gtataaagac ttcgcgctga 1980
85      taccagacgt tgcccgcata attacgaata tctgcacgcy cgaactgatc gttaaaactg 2040
86      cctggcacag caattgcccg gctttcttgt aacgcgcttt ccaccaacg ctgatcaatt 2100
87      ccacagtttt cgcgatccag actgaatgcc cacaggccgt cgagtttttt gatttcacgg 2160
88      gttggggttt ctacaggacg taccat 2186
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90 <211> LENGTH: 208
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Description of Artificial Sequence:5'UTR of

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95      Johnson mosaic virus
96      <400> SEQUENCE: 3
97      cgccccgggc ccaacacaaac acaacagaaac ctacgtcaat tgattttatc aatcgcaaag 60
98      ccttacaaaag atcttcgcag tcgttcatca acagattcac cgaaccattc ttgttagctc 120
99      tcgcacagag ataagcagga aacctgggca ggtgagtggg acacagtttg atagtaagag 180
100     aaaccagagg aagactgcag gtacccgc 208
101     <210> SEQ ID NO 4
102     <211> LENGTH: 1150
103     <212> TYPE: DNA
104     <213> ORGANISM: Artificial Sequence
105     <220> FEATURE:
106     <223> OTHER INFORMATION: Description of Artificial Sequence:Subterannean
107     clover virus S4 promoter with S7 enhancer
108     <400> SEQUENCE: 4
109     aatctgcagc ggccgcttaa tagtaattat gattaattat gagataagag ttgttattat 60
110     gcttatgagg aataaagaat gattaatatt gtttaatttt attccgcgaa gcggtgtgtt 120
111     atgtttttgt tggagacatc acgtgactct cacgtgatgt ctccgcgaca ggctggcacg 180
112     gggcttagta ttaccccggtg ccggatcaga gacatttgac taaatattga cttggaataa 240
113     tagcccttgg attagatgac acgtggacgc tcaggatctg tgatgctagt gaagcgctta 300
114     agctgaacga atctgacgga agagcggaca tacgcacatg gattatggcc cacatgtcta 360
115     aagtgtatct ctttacagct atattgatgt gacgtaagat gctttacttc gcttcgaagt 420
116     aaagtaggaa attgctcgct aagttattct tttctgaaaag aaattattta attctaatta 480
117     aattaaatga gtcgctataa atagtgtcga tgctgcctca catcgtattc ttcttcgcat 540
118     cgtctgttct ggttttaagc gggatccagg cctcgagata tcggtacctt gttattatca 600
119     ataaaagaat ttttattgtt attgtgttat ttggtaattt atgcttataa gtaattctat 660
120     gattaattgt gaattattaa gactaatgag gataataatt gaatttgatt aaattaactc 720
121     tgcgaagcta tatgtctttc acgtgagagt cacgtgatgt ctccgcgaca ggctggcacg 780
122     gggcttagta ttaccccggtg ccgggatcag agacatttga ctaaatgttg acttgggaata 840
123     atagcccttg gattagatga cacgtggacg ctcaggatct gtgatgctag tgaagcgctt 900
124     aagctgaacg aatctgacgg aagagcggac aaacgcacat ggactatggc ccactgcttt 960
125     attaaagaag tgaatgacag ctgtctttgc ttcaagacga agtaaagaat agtggaaaac 1020
126     gcgtaaagaa taagcgtaact cagtacgctt cgtggcttta tataaatagt gcttcgtctt 1080
127     attcttcggt gtatcatcaa cgaagaagtt aagctttgtt ctgcgtttta atgatcgatg 1140
128     gccagtcgac 1150
129     <210> SEQ ID NO 5
130     <211> LENGTH: 1052
131     <212> TYPE: DNA
132     <213> ORGANISM: Artificial Sequence
133     <220> FEATURE:
134     <223> OTHER INFORMATION: Description of Artificial Sequence: subterranean
135     clover virus promoter S4 with S4 enhancer
136     <400> SEQUENCE: 5
137     ggatccaggc ctcgagatat cggtaacctg ttattatcaa taaaagaatt tttattgtta 60
138     ttgtgttatt tggtaattta tgcttataag taattctatg attaatgttg aattattaaag 120
139     actaatgagg ataataattg aatttgatta aattaactct gcgaagctat atgtctttca 180
140     cgtgagagtc acgtgatgtc tccgcgacag gctggcacgg ggcttagtat taccctgtgc 240
141     cgggatcaga gacatttgac taaatgttga cttggaataa tagcccttgg attagatgac 300
142     acgtggacgc tcaggatctg tgatgctagt gaagcgctta agctgaacga atctgacgga 360
143     agagcggaca aacgcacatg gactatggcc cactgcttta ttaaagaagt gaatgacagc 420
144     tgtctttgct tcaagacgaa gtaaagaata gtggaaaacg cgtggatcca ggctctcgaga 480

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145      tatcgggtacc ttgttattat caataaaaaga attttttattg ttattgtgtt atttggtaat 540
146      ttatgcttat aagtaattct atgattaatt gtgaattatt aagactaatg aggataataa 600
147      ttgaatttga ttaaattaac tctgcgaagc tatatgtctt tcacgtgaga gtcacgtgat 660
148      gtctccgcga caggctggca cggggcttag tattaccccg tgccgggatc agagacattt 720
149      gactaaatgt tgacttgga taatagccct tggattagat gacacgtgga cgctcaggat 780
150      ctgtgatgct agtgaagcgc ttaagctgaa cgaatctgac ggaagagcgg acaaacgcac 840
151      atggactatg gccactgct ttattaaaga agtgaatgac agctgtcttt gcttcaagac 900
152      gaagtaaaga atagtggaaa acgcgtaaaag aataagcgta ctcagtacgc ttcgtggctt 960
153      tatataaata gtgcttcgtc ttattcttcg ttgtatcatc aacgaagaag ttaagctttg 1020
154      ttctgcgttt taatgatcga tggccagtcg ac 1052

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155 <210> SEQ ID NO 6
156 <211> LENGTH: 1583
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: coding
161      sequence of the desaturase CoP construct
162 <220> FEATURE:
163 <221> NAME/KEY: misc_feature
164 <222> LOCATION: (1)..(480)
165 <223> OTHER INFORMATION: corresponding to the 5' end of the
166      delta12-desaturase (fad2) coding region, in sense
167      orientation
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (1101)..(1583)
171 <223> OTHER INFORMATION: corresponding to the 5' end of the
172      delta12-desaturase (fad2) coding region, in anti
173      sense orientation
174 <400> SEQUENCE: 6

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175      atcattatag cctcatgctt ctactacgtc gccaccaatt acttctctct cctccctcag 60
176      cctctctctt acttggcttg gccactctat tgggcctgtc aaggetgtgt cctaactggg 120
177      atctgggtca tagccacga atgcggtcac cacgcattca gcgactacca atggctggat 180
178      gacacagttg gtcttatctt ccattccttc ctctcgtcc cttacttctc ctggaagtat 240
179      agtcatcgcc gtcaccattc caacactgga tccctcgaaa gagatgaagt atttgtccca 300
180      aagcagaaat cagcaatcaa gtggtacggg aaataacctca acaaccctct tggacgcac 360
181      atgatgttaa cgtccagtt tgtcctcggg tggcccttgt acttagcctt taacgtctct 420
182      ggcagaccgt atgacgggtt cgttgccat ttcttcccca acgtcccat ctacaatgac 480
183      cgagaacgcc tccagatata cctctctgat gcgggtattc tagccgtctg ttttggctct 540
184      taccgttacg ctgctgcaca agggatggcc tcgatgatct gctctacgg agtaccgctt 600
185      ctgatagtga atgcgttctt cgtcttgatc acttacttgc agcactca tccctcgttg 660
186      cctcactacg attcatcaga gtgggactgg ctccaggagg ctttggctac cgtagacaga 720
187      gactacggaa tcttgaacaa ggtgttccac aacattacag acacacacgt ggctcatcac 780
188      ctgttctcga caatgccgca ttataacgca atggaagcta caaaggcgat aaagccaatt 840
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190      aaggagtgtg tctatgtaga accggacagg gaagggtgaca agaaagggtg gtactgggtac 960
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192      ttttgttaaa gaagctatgc ttcgttttaa taatcttatt gtccattttg ttgtgttatg 1080
193      acattttggc tgctcattat gttcagtaac atctaccctc gcaaccctt ctttaccggt 1140
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195      tgtttgacct gccaatgtga gtactacgca ggttctccca acaactccat aaagggcatg 1260
196      gtgaactaac gactaaagac gaaaccctgt ttatgaagta gagaaagctc cctaggtcac 1320
197      aaccttacca ctgccgctac tgatatgaag gtccctcttca ttccctgctc ctccttcctt 1380
198      accttctatt ctggttgaca cagtaggtcg gtaaccatca gcgacttacg caccactggc 1440
199      gtaagcaccg gatactgggt ctatggtcaa tctgtgtcg gaactgtccg ggttatctca 1500
200      ccggttcggt tcattctctc tccgactccc tctctctctc tcattaacca ccgctgcac 1560
201      atcttcgtac tccgatatta cta 1583
202 <210> SEQ ID NO 7
203 <211> LENGTH: 786
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence: intron 2 of
208 the Flaveria trinervia purvate orthophosphate
209 dikinase
210 <400> SEQUENCE: 7
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212      gttaattagt atgattataa taatatagtt gttataattg tgaaaaaata atttataaat 120
213      atattgttta cataaacaac atagtaatgt aaaaaaatat gacaagtgat gtgtaagacg 180
214      aagaagataa aagttgagag taagtatatt attttttaatg aatttgatcg aacatgtaag 240
215      atgatatact agcattaata tttgttttaa tcataatagt aattctagct ggtttgatga 300
216      attaaatata aatgataaaa tactatagta aaaataagaa taaataaatt aaaataatat 360
217      ttttttatga ttaatagttt attatataat taaatatcta taccattact aaatatttta 420
218      gtttaaaagt taataaatat tttgttagaa attccaatct gcttgtaatt tatcaataaa 480
219      caaaatatta aataacaagc taaagtaaca aataatatca aactaataga aacagtaatc 540
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